

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/736,868  
Source: 1FWD  
Date Processed by STIC: 12/22/04

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## RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/10/736,868

TIME: 15:26:10

Input Set : A:\08451~1.txt

Output Set: N:\CRF4\12222004\J736868.raw

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3 <110> APPLICANT: Solomon, Aaron
4     Morimoto, Richard
5     Beitel, Greg
7 <120> TITLE OF INVENTION: OSR-1 Nucleic Acids and Proteins
9 <130> FILE REFERENCE: NWestern-08451
11 <140> CURRENT APPLICATION NUMBER: 10/736,868
12 <141> CURRENT FILING DATE: 2003-12-16
14 <160> NUMBER OF SEQ ID NOS: 6
16 <170> SOFTWARE: PatentIn version 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1932
20 <212> TYPE: DNA
21 <213> ORGANISM: Caenorhabditis elegans
23 <400> SEQUENCE: 1
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26 caatctccat cgacttccga tgctccggga gctttgttgt catctctcgt aggtaaaagc      120
28 catcaaaaac taccactggc tccatcaatg gaagctcttg aactgatggg tgttcaattt      180
30 gttgatgctc tcatcaaaaa aggtcaaatg gaaatggcaa aaggagcatt taagactcaa      240
32 ttagaagttc tagagaaagt acatcctgat caattcgata agtacaaaaa gctaaaagtt      300
34 gatgatttgg cagctgatgc agttatgcaa caggcggaga tggcaaaatt acagcctaaa      360
36 tcaggaaatg catttatcga tatgttgaat ggaaatggaa tccaatttgg tagcagtatt      420
38 cgtggattag aagatgctat ccgaacgcag agagatatgg aaaatacggg tccgtccgaa      480
40 cagattgcca aagccgtaat ggacaaattt caaacacaaa ttctcccagg actcgttgca      540
42 aatatgatcg ctggcaagaa cccctttaa atgcctcaac aaatgagaaa agctcaagct      600
44 gctccatcgt cagtgttcca acaagctctt gctcaaagag caatgttagg taaaaatgcc      660
46 ccagttgccg gtggaagagg tgaagaacaa cggatgatga tgaatcgagt ggaccaaaga      720
48 atgcaacaaa gagaacttca agaggaagat gaagatgatg atgatcttga ggacgaggat      780
50 gtaccagaaa gaagaagttc ggatggagaa ccacaaagtg aagcagagca tcagagaaga      840
52 gatttagcca ggagattgaa aagtagtcct agattaaaag agcttttaca gaatgcggaa      900
54 gttcaatcat tgctctctta ccaacgaatg agggattctc cactgagcaa gcgaaggcct      960
56 ttggctatga acgatgagga tgaaagtgca ttccgcgcaa tggaggctcg tgcaaaacta     1020
58 gatcaaaaaa ctcaacttgt gctcgggtctc catggttttg gagagtctga tgatgatgaa     1080
60 gacgaagaag atgaaaattt gattgatcca tctgaaaatt cattccgtcg tgcaccactt     1140
62 cgtctttctt ccggaattcg tgagaaatta aagtcaaag atgaattgaa aagtgcattg     1200
64 gacagaatta aatatcgagt tgatgacgtg gaaaagtatc ttgctccaaa gccgatggaa     1260
66 ttcaatccaa aacctcagcc tggctaattt gctccacgta aaatcccaac aagaccagt     1320
68 aaaatgcttc cattattaat tggatctgat ccaaaagtgc aagaggaaat acgaagacat     1380
70 ccaagtaccg aatggaaaat tgcaaaagaa tcaagagttt tgacaaattt gaagaataat     1440
72 ccaagtcttg ctgcattgtt catggatgat aaattagaga atacattgaa aggaaggcaa     1500
74 atgttaactg atgaacagaa aggtagaaca cgtgtcaaaa caattcgtgc attaccaaga     1560
76 ctgttcggtg caccaactgc aaaagctgaa atgattgatg caaaggattt ccaagatatt     1620
78 gaagaacgtc ccattcctcc attgttcttt gaaccaaag gaaggcatac gagattgaga     1680
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82 cttgatccaa ctatgccagc cttgaacacg gctttctoga ctcaggggag agcccgtagc 1800
84 gagtgggata ccatgttcaa aatcccgaa aactggaatc ctggagatga agttgggttc 1860
86 aaaatgaact caaaaaccaa acgattcgtt ggaggaaatg gagcatttga tatgcctgca 1920
88 ctgggattgt ag 1932
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103 20 25 30
106 Leu Ser Ser Leu Val Gly Lys Ser His Gln Lys Leu Pro Leu Ala Pro
107 35 40 45
110 Ser Met Glu Ala Leu Glu Leu Met Gly Val Gln Phe Val Asp Ala Leu
111 50 55 60
114 Ile Lys Lys Gly Gln Met Glu Met Ala Lys Gly Ala Phe Lys Thr Gln
115 65 70 75 80
118 Leu Glu Val Leu Glu Lys Val His Pro Asp Gln Phe Asp Lys Tyr Lys
119 85 90 95
122 Lys Leu Lys Val Asp Asp Leu Ala Ala Asp Ala Val Met Gln Gln Ala
123 100 105 110
126 Glu Met Ala Lys Leu Gln Pro Lys Ser Gly Asn Ala Phe Ile Asp Met
127 115 120 125
130 Leu Asn Gly Asn Gly Ile Pro Ile Gly Ser Ser Ile Arg Gly Leu Glu
131 130 135 140
134 Asp Ala Ile Arg Thr Gln Arg Asp Met Glu Asn Thr Asp Pro Ser Glu
135 145 150 155 160
138 Gln Ile Ala Lys Ala Val Met Asp Lys Phe Gln Thr Gln Ile Leu Pro
139 165 170 175
142 Gly Leu Val Ala Asn Met Ile Ala Gly Lys Asn Pro Phe Lys Met Pro
143 180 185 190
146 Gln Gln Met Arg Lys Ala Gln Ala Ala Pro Ser Ser Val Phe Gln Gln
147 195 200 205
150 Ala Leu Ala Gln Arg Ala Met Leu Gly Lys Asn Ala Pro Val Ala Gly
151 210 215 220
154 Gly Arg Gly Glu Glu Gln Arg Met Met Met Asn Arg Val Asp Gln Arg
155 225 230 235 240
158 Met Gln Gln Arg Glu Leu Gln Glu Glu Asp Glu Asp Asp Asp Asp Leu
159 245 250 255
162 Glu Asp Glu Asp Val Pro Arg Arg Arg Ser Ser Asp Gly Glu Pro Gln
163 260 265 270
166 Ser Glu Ala Glu His Gln Arg Arg Asp Leu Ala Arg Arg Leu Lys Ser
167 275 280 285
170 Ser Pro Arg Leu Lys Glu Leu Leu Gln Asn Ala Glu Val Gln Ser Leu
171 290 295 300
174 Leu Ser Tyr Gln Arg Met Arg Asp Ser Pro Leu Ser Lys Arg Arg Pro
175 305 310 315 320

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182 Arg Ala Lys Leu Asp Gln Lys Ser Gln Leu Val Leu Gly Leu His Gly
183           340           345           350
186 Phe Gly Glu Ser Asp Asp Asp Glu Asp Glu Glu Asp Glu Asn Leu Ile
187           355           360           365
190 Asp Pro Ser Glu Asn Ser Phe Arg Arg Ala Pro Leu Arg Leu Ser Ser
191           370           375           380
194 Gly Phe Val Glu Lys Leu Lys Ser Asn Asp Glu Leu Lys Ser Ala Leu
195 385           390           395           400
198 Asp Arg Ile Lys Tyr Arg Val Asp Asp Val Glu Lys Tyr Leu Ala Pro
199           405           410           415
202 Lys Pro Met Glu Phe Asn Pro Lys Pro Gln Pro Gly Tyr Phe Ala Pro
203           420           425           430
206 Arg Lys Ile Pro Thr Arg Pro Arg Lys Met Leu Pro Leu Leu Ile Gly
207           435           440           445
210 Ser Asp Pro Lys Val Gln Glu Glu Ile Arg Arg His Pro Ser Thr Glu
211           450           455           460
214 Trp Lys Ile Ala Lys Glu Ser Arg Val Leu Thr Asn Leu Lys Asn Asn
215 465           470           475           480
218 Pro Ser Leu Ala Ala Leu Phe Met Asp Asp Lys Leu Glu Asn Thr Leu
219           485           490           495
222 Lys Gly Arg Gln Met Leu Thr Asp Glu Gln Lys Gly Arg Thr Arg Val
223           500           505           510
226 Lys Thr Ile Arg Ala Leu Pro Arg Leu Phe Gly Ala Pro Thr Ala Lys
227           515           520           525
230 Ala Glu Met Ile Asp Ala Lys Val Phe Gln Asp Ile Glu Glu Arg Pro
231           530           535           540
234 Ile Pro Pro Leu Phe Phe Glu Pro Lys Gly Arg His Thr Arg Leu Arg
235 545           550           555           560
238 Trp Thr Gly Ala Asn Glu Lys Glu Ile Pro Gly Leu Gly Ser Arg Phe
239           565           570           575
242 Ile Leu Pro Ser Leu Asp Pro Thr Met Pro Ala Leu Asn Thr Ala Phe
243           580           585           590
246 Ser Thr Gln Gly Arg Ala Arg Asp Glu Trp Asp Thr Met Phe Lys Ile
247           595           600           605
250 Pro Asn Asn Trp Asn Pro Gly Asp Glu Val Gly Phe Lys Met Asn Ser
251           610           615           620
254 Lys Thr Lys Arg Phe Val Gly Gly Asn Gly Ala Phe Asp Met Pro Ala
255 625           630           635           640
258 Leu Gly Leu
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263 <211> LENGTH: 2993
264 <212> TYPE: DNA
265 <213> ORGANISM: Caenorhabditis elegans
267 <400> SEQUENCE: 3
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272 cgtccgctac tactgtatct tctggacatc tacctgtata cacaccagtg gccagtcac      180

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274 tgccattaca atttcatcaa ttgacacttc ttcaacaaca accgccgtcc tcattcactc 240
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278 tggagatgct ggtagatcag ggaactgatg catcgtcac cgcctccacg tccacctcat 360
280 ctgtttcagc attcggagcg gacacgttca tgaatacacc ggatgatgtg atgatgaatg 420
282 atgatatgga accgattcct cgtgatcggt gcaatacgtg gccaatgcgt aggccgcaac 480
284 tcgaaccacc actcaactcg agtcccatta ttcatagaaca aattcctgaa gaagatgctg 540
286 acctatacgg gagcaatgag caatgtggac agctcggcgg agcatcttca aacgggtcga 600
288 cagcaatgct tcatactcca gatggaagca attctcatca gacatcgttt ccttcggaaa 660
290 tgtccgaatc gccagacgat accgtatcgg gaaaaaagac aacgaccaga cggaaacgctt 720
292 ggggaaatat gtcatatgct gaacttatca ctacagccat tatggctagt ccagagaaac 780
294 ggtaaactct tgcacaagtt tacgaatgga tgggtccagaa tgttccatac ttcagggata 840
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298 attctcgttt catgccgaatt cagaatggaag gagccggaaa gagctcgtgg tgggttatta 960
300 atccagatgc aaagccagga aggaatccac ggcgtacacg tgaacgatcc aatactattg 1020
302 agacgactac aaaggctcaa ctcgaaaaat ctgcgcggcg agccaagaag aggataaagg 1080
304 agagagcatt gatgggctcc cttcaactcga cacttaatgg aaattcgatt gccggatcga 1140
306 ttcaaacgat ttctcacgat ttgtatgatg atgattcaat gcaaggagca tttgataacg 1200
308 ttccatcatc tttccgtccc cgaactcaat cgaacctctc gattcctgga tcgtcgtctc 1260
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316 aaccaattgc tccaccacca tcataccacg agttgaacag tgtccgtgga tcgtgtgctc 1500
318 agaatccact tcttcgaaat ccaattgtgc caagcactaa cttcaagcca atgccactac 1560
320 cgggtgccta tggaaactat caaaatggtg gaataactcc aatcaattgg ctatcaacat 1620
322 ccaactcatc tccactgcct ggaattcaat cgtgtggaat tgtagctgca cagcatactg 1680
324 tcgtctcttc atcggctcct ccaattgatt tggaaaatct gacacttccc gatcagccac 1740
326 tgatggatac tatggatggt tatgcatgta tcagacatga gctgagtcaa gctggagggc 1800
328 agcatattca ttttgatttg taaattctct tcattttggt tcccctggtg ttgttcgaaa 1860
330 gagagatagc aaagcagcga ggagtggaga atcttcgctc ttcattcttt caaatcccta 1920
332 ctacacaca ctcaacgatc atcacagcca gaccatcaat attcttccaa attttgacgt 1980
334 cgtaattttt ttttcagttt tttcaaaaac tctattttct attttctgtc gtttggtccc 2040
336 ctttctctcg tctaattcca acacattcat cccagtgaag tcgtgtaata ataataaaa 2100
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356 ttcaaaaaat ctcagtttta aatgggtggg caatatatcg gatccccctc tacaccagaa 2700
358 cagtcttgca atttcagaga atgattttca gatttttcat atcacaggcc cccttttttt 2760
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362 tgttatcctg tacattttcc ttccaattct ttctggctat ttctgatttt cgagttcata 2880
364 ttctctacgt ctcactttct ctgcgcccac gccccctttt tcgtctccct ccgcccccaa 2940
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369 <210> SEQ ID NO: 4
370 <211> LENGTH: 530

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371 <212> TYPE: PRT
372 <213> ORGANISM: Caenorhabditis elegans
374 <400> SEQUENCE: 4
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380 Cys Tyr Thr Trp Pro Met Gln Gln Tyr Ile Tyr Gln Glu Ser Ser Ala
381 20 25 30
384 Thr Ile Pro His His His Leu Asn Gln His Asn Asn Pro Tyr His Pro
385 35 40 45
388 Met His Pro His His Gln Leu Pro His Met Gln Gln Leu Pro Gln Pro
389 50 55 60
392 Leu Leu Asn Leu Asn Met Thr Thr Leu Thr Ser Ser Gly Ser Ser Val
393 65 70 75 80
396 Ala Ser Ser Ile Gly Gly Gly Ala Gln Cys Ser Pro Cys Ala Ser Gly
397 85 90 95
400 Ser Ser Thr Ala Ala Thr Asn Ser Ser Gln Gln Gln Gln Thr Val Gly
401 100 105 110
404 Gln Met Leu Ala Ala Ser Val Pro Cys Ser Ser Ser Gly Met Thr Leu
405 115 120 125
408 Gly Met Ser Leu Asn Leu Ser Gln Gly Gly Gly Pro Met Pro Ala Lys
409 130 135 140
412 Lys Lys Arg Cys Arg Lys Lys Pro Thr Asp Gln Leu Ala Gln Lys Lys
413 145 150 155 160
416 Pro Asn Pro Trp Gly Glu Glu Ser Tyr Ser Asp Ile Ile Ala Lys Ala
417 165 170 175
420 Leu Glu Ser Ala Pro Asp Gly Arg Leu Lys Leu Asn Glu Ile Tyr Gln
421 180 185 190
424 Trp Phe Ser Asp Asn Ile Pro Tyr Phe Gly Glu Arg Ser Ser Pro Glu
425 195 200 205
428 Glu Ala Ala Gly Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu His
429 210 215 220
432 Ser Arg Phe Met Arg Ile Gln Asn Glu Gly Ala Gly Lys Ser Ser Trp
433 225 230 235 240
436 Trp Val Ile Asn Pro Asp Ala Lys Pro Gly Arg Asn Pro Arg Arg Thr
437 245 250 255
440 Arg Glu Arg Ser Asn Thr Ile Glu Thr Thr Thr Lys Ala Gln Leu Glu
441 260 265 270
444 Lys Ser Arg Arg Gly Ala Lys Lys Arg Ile Lys Glu Arg Ala Leu Met
445 275 280 285
448 Gly Ser Leu His Ser Thr Leu Asn Gly Asn Ser Ile Ala Gly Ser Ile
449 290 295 300
452 Gln Thr Ile Ser His Asp Leu Tyr Asp Asp Asp Ser Met Gln Gly Ala
453 305 310 315 320
456 Phe Asp Asn Val Pro Ser Ser Phe Arg Pro Arg Thr Gln Ser Asn Leu
457 325 330 335
460 Ser Ile Pro Gly Ser Ser Ser Arg Val Ser Pro Ala Ile Gly Ser Asp
461 340 345 350
464 Ile Tyr Asp Asp Leu Glu Phe Pro Ser Trp Val Gly Glu Ser Val Pro
465 355 360 365

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/736,868

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